



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/047,412
Source: 61PE
Date Processed by STIC: 2/2/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY, or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

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O I P E

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/047,412

DATE: 02/07/2002
TIME: 07:30:42

Input Set : A:\EP.txt
Output Set: N:\CRF3\02072002\J047412.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Levin, Joshua Z.
4 Budziszewski, Gregory J.
5 Potter, Sharon L.
6 Wegrich, Lynette M.
7 . 8 <120> TITLE OF INVENTION: Herbicide Target Genes and Methods
8 . 9 <130> FILE REFERENCE: PB/5-30780DIV1
10 10 <140> CURRENT APPLICATION NUMBER: US/10/047,412
11 11 <141> CURRENT FILING DATE: 2002-01-14
12 12 <160> NUMBER OF SEQ ID NOS: 29
13 13 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

1207 <210> SEQ ID NO: 18
1208 <211> LENGTH: 218
1209 <212> TYPE: DNA
1210 <213> ORGANISM: Arabidopsis thaliana
1211 <400> SEQUENCE: 18 → see item 9 on Env
E--> 1213 aatatggaa aacatggatc aagtcttgc aagccgagca ctaaaaagtgt aaaaatgaac 60
1214 caaagggtgaa aagaaactgc tttctctatc tcatagtctgt ttaagggttt cttcggtcac 120
1215 ttaagagaca aaaggcattg ttttgcac tctttggaaa cgtttataaa attttatttt 180
1216 tgtatttagag ccaaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 218
1653 <210> SEQ ID NO: 29
1654 <211> LENGTH: 477
1655 <212> TYPE: PRT
1656 <213> ORGANISM: Arabidopsis thaliana
1658 <400> SEQUENCE: 29
1659 Met Met Thr Leu Asn Ser Leu Ser Pro Ala Glu Ser Lys Ala Ile Ser
1660 1 5 10 15
1661 Phe Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly
1662 20 25 30
E--> 1663 Phe Ser Leu Arg Arg Arg Xaa Gln Gly Arg Gly Phe Gly Lys Gly Val
1664 35 40 45
1665 Lys Cys Ser Val Lys Val Gln Gln Gln Gln Pro Pro Pro Ala Trp
1666 50 55 60
E--> 1667 Pro Gly Arg Ala Xaa Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro
1668 65 70 75 80
E--> 1669 Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Xaa Xaa Gly Thr Gln Thr
1670 85 90 95
1671 Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu
1672 100 105 110
1673 Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe
→ see item 9 on Env
summary sheet
see item 9 on Env
summary sheet
see item 9 on Env
summary sheet

Input Set : A:\EP.txt
Output Set: N:\CRF3\02072002\J047412.raw

1674 115 120 125
E--> 1675 Lys Pro Xaa Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu
1676 130 135 140
E--> 1677 Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Xaa Glu Ile Ile Pro Gly
1678 145 150 155 160
E--> 1679 Glu Xaa Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val
1680 165 170 175
E--> 1681 Val Thr Gly Ile Val Gly Cys Ala Gly Leu Xaa Pro Thr Val Ala Ala
1682 180 185 190
1683 Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile
1684 195 200 205
1685 Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys
1686 210 215 220
1687 Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln
1688 225 230 235 240
1689 Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly
1690 245 250 255
1691 Gly Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val
1692 260 265 270
1693 Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr
1694 275 280 285
1695 Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala
1696 290 295 300
1697 His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His
1698 305 310 315 320
E--> 1699 Xaa Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val
1700 325 330 335
1701 Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr
1702 340 345 350
E--> 1703 Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Xaa Arg
1704 355 360 365
1705 Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn
1706 370 375 380
1707 Val Lys Tyr Pro Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly
1708 385 390 395 400
1709 Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu
1710 405 410 415
1711 Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val
1712 420 425 430
1713 Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser
1714 435 440 445
1715 Leu Glu Glu Ile Val His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala
1716 450 455 460
E--> 1717 Xaa Val Gln Leu Ser Ser Gly Ala Arg Pro Val His Ala
1718 465 470 475
E--> 1728 1
E--> 1730 1

item 9 *item 9* *item 9* *item 9*

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/047,412

DATE: 02/07/2002
TIME: 07:30:43

Input Set : A:\EP.txt
Output Set: N:\CRF3\02072002\J047412.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1213 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:1541 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:1541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1549 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:1549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1553 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:1553 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1565 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:1565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1569 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:1569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1573 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:1573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1577 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:1577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1613 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:1613 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1621 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:1621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1649 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:1649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1663 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:29
M:340 Repeated in SeqNo=29
L:1728 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:29
M:332 Repeated in SeqNo=29

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 10/047412

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping".

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial-Sequence

11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.